

USE OF YNES, ESSENTIAL BACTERIAL GENES AND  
POLYPEPTIDES

1 ATGATTACAATAGTTTATAATTCTAGGCCATCTGGCTGGTTGGATTCCATCTGGTCTCTGGATTCAACAGTTATTCTTCAMTCAAATCTACGGGAGC 100  
TACTAATGTTATCAAATAATTAGGATCGGATAGACGGACCCAAAGCTTAAGGTAGACCGAGACCTAACCTGTTAGTTAGATGGCTCG  
1 M I T I V L L I L A Y L L G S I P S G L W I G O V F F O I N L R E H 14  
101 ATGGTTCTGGTAACACTGGAACCGACCAACACCTTCCGCATTAGGTAAAGAAAGCTGGTATGGCAAACCTTTGATTGACTTTTCAAAGGAACCCCTAGC 200  
TACCAAGACCATTTGTGACCTTGCTGGTTGGAAAGGGTAAAGCTGAAACACTAACTGAAAAGCTTCCCTGGATCG  
35 G S G N T G T T N T F R I L G K A G M A T F V I D F F K G T L A 67  
201 AACGGCTGCTTCCGATTATTTCTACAGGGCTTCTCCTCTCATCTTGGACTTTGGCTGTATCGGCCATACCTCCCTATCTCTGGAGGATT 300  
TTGGGACGAACGGCTAAATAAAAAGTAGATGTTCGGCAAAGAGGAGGTAGAAACCTGAAACCGACATAAGCCGGATAGAAAAGCTGGCTCAA  
68 T L L P I I F H L Q G V S P L I F G L L A V I G H T F P I F A G F 100  
301 AAAGGTGGTAAGGCTGTCGCAACCAAGTGGCTGTTGGAGGTAGTTGGCTATCTCTGTCTCACCTGGATTATCTCTGGAGCTCTATC 400  
TTTCCACCATTCCGACAGCGTTGGTCAGGACCTCACTAAAGCCTAAACGGCTAAAGCAAGAGATGGAAACGCCATAAGAAGAAAACCTCGAGAGATAG  
101 K G G K A V A T S A G V I F G F A P I F C L Y L A I I F F G A L Y L 134  
401 TTGGCAGTATGATTCACTGTCTAGTGTCAAGGCATCGATTGGGGTGTATTCGGGCTCTGGCTTTGGTTTATCCCTGAGTAACCTATGA 500  
ACCGGTCACTAAACTGACAGATCACAGTGTCTAGTAACGCCGACATAAGCCCCAAGACGAGAAAAGGTGAAAACCAAATAGGACTCATGGATACT  
135 G S M I S L S S V T A S I A A V I G V L L F P L F G F I L S N Y D 167  
501 CCTCTCTCTCATGGCTTAACTTCTAGGACTCTGGCTAGTTGATTATCATTCAGGACATAAGGACATAAGGAGTATGGCTGATCAAATAAAACTGAAAATTGGTC 600  
GGAACCCCTAACCTGGATTGGTAGTTAGGATCTAGTTGAGGATAGTGAACGATCAGTGTGTTATCGAGGATAGTTGACTTTGACTTTAAACCGAG  
168 S L F I A I I L A S L I I R H K D N I A R I K N K T E N L V 200  
601 CCTTGGGGATTGAACTTAACCCATCAAGATCCTAAAAAATAA 642 SEQ ID NO:2  
GGAACCCCTAACCTGGATTGGTAGTTAGGATCTAGGATTTTATT SEQ ID NO:11  
201 P W G L N L T H Q D P K K • 213 SEQ ID NO:1

FIG. 1

Applicant(s): Christian Fritz et al.

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1 M I T I V L L I L A Y L L G S I P S G L W I G O V F F O I N L R E H 34  
 101 ATGGATTCAAAATAGTTTATTAACTCCTAGCCCTATCTGGTGGGCTCATCTGGATTCTGGATTCACAGTTCTACAGTTCTAAGGTTAGATGGCTCG  
 TACTAATGTTTATCAAATAATTAGGATCGGATAGACCAAGCTAAGGTAGACCAGACCTAACCTGTTACAAGGTTAGATGGCTCG  
 101 ATGGTTCTGGTAACACTGGAACGCCAACACCTTCGGCATTTAGGTAAGAAAAGCTGGTATGGCACACCTTTGGATTGACTTTTCAAGGAAACCCCTAGC  
 TACCAAGACCATTGTGACCTTGCTGGTTGCTGGTAAAGGGTAAATCCATTCTTGACCCATACCGGTGGAAACACTAACTGAAAAGTTCTGGGATCG  
 35 G S G N T G T T N T F R I L G K K A G M A T F V I D F F K G T L A 67  
 201 AACGCTGGCTTCGGATTATTTTCATCTACAGGGCTTCTCCTCTCATCTGGACTTTGGCTGTTATCGGCCATACCTTCCTATCTTGGCAGGATT  
 TTGGACGGAAAGGCTTAATAAAAGTAGATGTTAGATGTTAGGAGGTAGAAAGAGGAAGGGATAGAAACCTGAAACCGACAATAGCCGGTATGGAAAGGGT  
 68 T L L P I I F H L Q G V S P L I F G L L A V I G H T F P I F A G F 100  
 301 AAAGGTGGTAAGGGCTGTCGCAACCAACGGCTGGAGTGATTTCGGATTTCGGCTATCTTCTGTCTCATCTTGCGATTATCTCTGGCTCTCTATC  
 TTCCACCATTCGACAGGGTGGTCAGACCCCTCAAAAGCTAAACGGQATAGAAAGACAGAGATGGAAACGCTAATAAGAAGAACCTCGAGAGATAG  
 101 K G G K A V A T S A G V I F G F A P I F C L Y L A I I F F G A L Y L 134  
 401 TTGGCAGATTGATTCACTGTCTAGTGTCAAGGATCTGATTGGGGCTGTTATCGGGGTTCTGCTCTTCCACTTTGGTTTATCTGAGTAACTATGA  
 AACCGTCATACTAAAGTGACAGATCACAGTGACAGATCAAGTGACAGATCAAGTGACAGATCAAGTGACAGATCAAGTGACAGATCAAGTGACAGAT  
 135 G S M I S L S S V T A S I A A V I G V L L F P L F G F I L S N Y D 167  
 501 CTCTCTCTCATCGCTATTATCTTAGGCACTTGCTAGTTGATTATCATTCTGCTATAAGGACAATAAGCTGTATCAAAAATAACTGAAAATTGGTC  
 GAGAGAAAGTAGGATAATGAATCGTGAACGATCAAATAGTAAGCAGTCAAGTGTCGTAAGCTAACACTAACTGAGTAACTGAGTAACTGAGT  
 168 S L F I A I I L A L A S L I I I R H K D N I A R I K N K T E N L V 200  
 601 CCTGGGGATTGAAACCTAACCCCTAACAGATCCAAANAAATA 642 SEQ ID NO:2  
 GGAAACCCCTAACCTGGATTGGTAGTTCTAGGATTTTTATT 642 SEQ ID NO:11  
 201 P W G L N L T H Q D P K K • 213 SEQ ID NO:1

EIG

SEQ ID NO:1